was determined that *VTC1* is centromere distal to nga168 and m429. All seven *vtc1/vtc1* mapping lines that were recombinant between nga168 and *VTC1* were also recombinant for marker 178 (including two between m429 and nga168), indicating that the relative order of these loci is as shown. This map is inconsistent with public domain recombinant inbred results, presumably because of the limited resolution of the recombinant inbred map: m429 is reported as being centromere proximal to nga168 (nasc.nott.ac.uk/new_ri_map.html). Our mapping data place *VTC1* within a 2 Mb region on Chr 2 that spans m429 to just beyond marker m336, which is currently being sequenced by the Institute for Genomic Research (TIGR). The sequence of a 92 kb BAC (T5I7) within that contig (Figure 3B) was annotated by TIGR and the open reading frame T5I7.7 was identified as a putative mannose-1-phosphate guanyltransferase (www.tigr.org/docs/tigr-scripts/bac_scripts/bac_display.spl?bac_ name=T5I7). An alias for this enzyme is GDP-mannose pyrophosphorylase, which catalyzes step 4 in the proposed AsA biosynthetic pathway shown in Fig. 1. In this reaction, mannose-1-P is converted to GDP-mannose, with the consumption of GTP and the release of inorganic pyrophosphate (PPi).

Please replace the entire paragraph beginning at page 11, line 29, and continuing through page 12, line 12, with the following replacement paragraph:

The mutant alleles *vtc1-1* and *vtc1-2* were sequenced from PCR-amplification products of genomic DNAs. For each mutant allele, an ~1.4 kb BglII fragment containing the majority of the coding region was sequenced using the primers, 5' TGGTAAATACGCACTCAAT 3' (SEQ ID NO: 1, named 5'-GMP) and 5' AAAACAGCAAACGACCCTAACAA 3' (SEQ ID NO: 2, named 3'-GMP). To confirm the public domain sequence of BAC T5I7 that included the base mutated in the *vtc1* alleles, both strands of a portion of a Col-0 wildtype *VTC1* ClaI genomic clone (described below) were sequenced. The sequence of *VTC1*, *vtc1-1*, and *vtc1-2* that included exon 1 and intron 1 was obtained directly from genomic DNA amplified with 5'-GMP and 5' CATTCTTGTTGGAGGCTTCGG 3' (SEQ ID NO: 3). The sequence downstream of the BglI fragment for *vtc1-1* and *vtc1-2* was obtained from genomic DNA amplified with the 5' GAATAAGCATCAATCAAAACGC 3' (SEQ ID NO: 4) and 5' GCTAAGACCGACTTCAATCG 3' (SEQ ID NO: 5). More than one independent PCR product was sequenced to confirm the veracity of the data.

A marked up copy of the foregoing replacement paragraphs, showing all of the changes relative to the previous versions of said paragraphs, is attached hereto on a separate page, in compliance with 37 C.F.R. 1.121(b).